

SEQUENCE LISTING

<110> FUKATSU et al.

<120> RECEPTOR FUNCTION REGULATING AGENT

<130> 20039.0005USWO

<140> US 10/580,906

<141> 2006-05-26

<150> PCT/JP2004/017996

<151> 2004-11-26

<150> JP 2003-394848

<151> 2003-11-26

<160> 20

<170> PatentIn Version 3.1

<210> 1

<211> 361

<212> PRT

<213> Human

<400> 1

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Met Ser Pro Glu Cys Ala Arg Ala Ala Gly Asp Ala Pro Leu Arg Ser
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Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys
      20              25              30
Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val
      35              40              45
Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
      50              55              60
Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn
      65              70              75              80
Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu
      85              90              95
Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His
      100             105             110
Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr
      115             120             125
Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln
      130             135             140
Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala
      145             150             155             160
Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe
      165             170             175
Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser
      180             185             190
Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp
      195             200             205
Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
      210             215             220
Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
      225             230             235             240

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cttacgctga gcttggcata ctctgagagc caccagatcc gagtgtccca acaagactac 780
cgactcttcc gcacgctctt cctgctcatg gtttccttct tcatcatgtg gagtcccatc 840
atcatcacca tcctcctcat cttgatccaa aacttccggc aggacctggg catctggcca 900
tcccttttct tctgggtggt ggccttcacg tttgccaact ctgccctaaa ccccatactg 960
tacaacatgt cgctgttcag gaacgaatgg aggaagattt tttgctgctt cttttttcca 1020
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Pro Asp Gln Val Asn Arg Thr His Phe Pro Phe Phe Ser Asp Val Lys
          20              25              30

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Gly Asp His Arg Leu Val Leu Ser Val Leu Glu Thr Thr Val Leu Gly
 35 40 45
 Leu Ile Phe Val Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
 50 55 60
 Val Val Arg Arg Arg Arg Gly Ala Thr Val Ser Leu Val Leu Asn
 65 70 75 80
 Leu Phe Cys Ala Asp Leu Leu Phe Thr Ser Ala Ile Pro Leu Val Leu
 85 90 95
 Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Val Cys His
 100 105 110
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 115 120 125
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 130 135 140
 Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala Ala Leu Leu Ala
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 Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro Leu Cys Ile Leu
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 Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp Gln Glu Ile Pro
 180 185 190
 Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu Ile Ser Trp Asp
 195 200 205
 Val Phe Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
 210 215 220
 Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
 225 230 235 240
 Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
 245 250 255
 Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
 260 265 270
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 275 280 285
 Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
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 Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
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 Tyr Asn Met Ser Leu Phe Arg Ser Glu Trp Arg Lys Ile Phe Cys Cys
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